

STN SEARCH HISTORY

ZH
9/15/06

=> d his

(FILE 'HOME' ENTERED AT 16:42:02 ON 15 SEP 2006)

FILE 'MEDLINE, EMBASE, BIOSIS, SCISEARCH, DISSABS, TOXCENTER' ENTERED AT
16:42:27 ON 15 SEP 2006

```
L1      173 S (KAPELLER-LIBERMANN R?/AU) OR (LIBERMANN R?/AU) OR (KAPELLER
L2      1 S L1 AND 47174
L3      1 S L1 AND GLYCOSYLTRANSFERASE
L4      0 S L1 AND (UDP-GALNAC? OR GALNAC? OR PPGALNAC?)
L5      0 S L1 AND (ACETYLGALACTOSAMINE? OR GALACTOSAMINE?)
L6      1 S L2 OR L3
L7      4 S GALNAC-T9 OR GALNACT9 OR UDP-GALNAC-T9 OR UDP-GALNACT9
L8      0 S PPGALNAC-T9 OR PPGALNACT9 OR UDP-PPGALNAC-T9 OR UDP-PPGALNACT
L9      1 S GALNAC? AND (TRANSFERASE (2A) 9)
L10     1 S GALNAC? AND (TRANSFERASE (2A) (9 OR T9 OR T-9))
L11     7 S GALNAC? AND (TRANSFERASE (5A) (9 OR T9 OR T-9))
L12     25 S GALNAC? AND (TRANSFERASE AND (T9 OR T-9))
L13     30 S L7 OR L9 OR L10 OR L11 OR L12
L14     9 DUP REM L13 (21 DUPLICATES REMOVED)
L15     1 DUP REM L7 (3 DUPLICATES REMOVED)
L16     7 S PPGANTASE-T9
L17     3 DUP REM L16 (4 DUPLICATES REMOVED)
L18     3 S PPGALNAC AND (T9 OR T-9 OR TRANSFERASE-9)
L19     3 S PPGALNAC? AND (T9 OR T-9 OR TRANSFERASE-9)
L20     15 S PPGANTASE? AND (T9 OR T-9 OR TRANSFERASE-9)
L21     18 S L19 OR L20
L22     6 DUP REM L21 (12 DUPLICATES REMOVED)
```

=> log y

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: August 16, 2006, 00:37:10 ; Search time 195 Seconds
(without alignments)
1413.854 Million cell updates/sec

Title: US-10-713-345-2
Perfect score: 3190
Sequence: 1 MAVARKIRTLTLVNILVFVG.....VQRCSGQKWMIRNWKHARH 603

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	3190	100.0	603	6	ABG73283	Abg73283 Human 471
2	3190	100.0	603	7	ADC77653	Adc77653 Human 471
3	3190	100.0	603	8	ADM46166	Adm46166 Human 471
4	2052.5	64.3	598	5	ABG32380	Abg32380 Novel hum
5	2052.5	64.3	598	5	ABP53502	Abp53502 Human pp-
6	2047.5	64.2	598	7	ADC35390	Adc35390 Human N-a
7	2044.5	64.1	598	8	ADS10894	Ads10894 Human the
8	2037	63.9	402	4	AAM40398	Aam40398 Human pol
9	1996.5	62.6	560	4	AAM41675	Aam41675 Human pol
10	1732	54.3	468	7	ADE47680	Ade47680 Human NOV
11	1732	54.3	468	8	ADJ78950	Adj78950 Human NOV
12	1732	54.3	468	8	ADJ71667	Adj71667 Human NOV
13	1732	54.3	468	8	ADJ71669	Adj71669 Human NOV
14	1732	54.3	468	8	ADJ71661	Adj71661 Human NOV
15	1731	54.3	468	8	ADJ71665	Adj71665 Human NOV
16	1727	54.1	315	4	AAM42184	Aam42184 Human pol
17	1625	50.9	435	8	ADJ71663	Adj71663 Human NOV
18	1586	49.7	607	5	AAE22155	Aae22155 Human TRN
19	1586	49.7	607	6	ADA54308	Ada54308 Human pro
20	1586	49.7	607	7	ADC35389	Adc35389 Human N-a
21	1571	49.2	607	7	ADE47686	Ade47686 Human NOV
22	1571	49.2	607	7	ADE47688	Ade47688 Human NOV
23	1571	49.2	607	7	ADE47690	Ade47690 Human NOV
24	1571	49.2	607	8	ADJ78958	Adj78958 Human NOV
25	1571	49.2	607	8	ADJ78956	Adj78956 Human NOV
26	1571	49.2	607	8	ADJ78960	Adj78960 Human NOV
27	1478	46.3	407	4	ABB15037	Abb15037 Human ner
28	1474	46.2	354	6	ADA54187	Ada54187 Human pro
29	1431	44.9	266	3	AAB41739	Aab41739 Human ORF
30	1118	35.0	358	4	AAM40865	Aam40865 Human pol
31	1118	35.0	358	8	ADS12137	Ads12137 Human the
32	1085	34.0	297	7	ADB64287	Adb64287 Human pro
33	1085	34.0	297	8	ADQ66754	Adq66754 Novel hum
34	1077	33.8	297	7	ADM04203	Adm04203 Human pro
35	1077	33.8	297	9	AEC87133	Aec87133 Human cDN
36	1076	33.7	297	4	AAM39079	Aam39079 Human pol
37	949	29.7	177	7	ADE25972	Ade25972 N-acetylgl
38	949	29.7	177	9	ADX58133	Adx58133 Human pol
39	949	29.7	177	9	ADX58235	Adx58235 Human pol
40	939	29.4	571	7	ADC10116	Adc10116 Human NOV
41	931.5	29.2	556	5	ABG32379	Abg32379 Novel hum
42	931.5	29.2	556	7	ADE25918	Ade25918 Novel N-a

PRINT OUT OF
SEQUENCE
SEARCH
RESULTS

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9/15/06

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: August 16, 2006, 00:47:04 ; Search time 51 Seconds
(without alignments)
1034.921 Million cell updates/sec

Title: US-10-713-345-2
Perfect score: 3190
Sequence: 1 MAVARKIRTLTLTNILVFVG.....VQRCSGQKWMIRNWIKHARH 603

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3190	100.0	603	2	US-09-973-457-2	Sequence 2, Appli
2	1586	49.7	607	2	US-10-094-749-1876	Sequence 1876, Ap
3	1474	46.2	354	2	US-10-094-749-1755	Sequence 1755, Ap
4	1085	34.0	297	2	US-10-104-047-2441	Sequence 2441, Ap
5	906.5	28.4	517	1	US-08-967-508-19	Sequence 19, Appl
6	906.5	28.4	517	2	US-08-967-506-19	Sequence 19, Appl
7	906.5	28.4	517	5	PCT-US94-02552-19	Sequence 19, Appl
8	906.5	28.4	559	1	US-08-967-508-9	Sequence 9, Appli
9	906.5	28.4	559	2	US-08-967-506-9	Sequence 9, Appli
10	906.5	28.4	559	5	PCT-US94-02552-9	Sequence 9, Appli
11	844	26.5	578	2	US-10-074-527-8	Sequence 8, Appli
12	836	26.2	578	2	US-09-217-306B-2	Sequence 2, Appli
13	833	26.1	560	2	US-09-217-306B-10	Sequence 10, Appl
14	782.5	24.5	581	2	US-10-074-527-2	Sequence 2, Appli
15	761	23.9	552	2	US-10-104-047-2405	Sequence 2405, Ap
16	757	23.7	633	1	US-08-648-298-2	Sequence 2, Appli
17	744	23.3	603	2	US-09-795-926-43	Sequence 43, Appl
18	744	23.3	603	2	US-10-364-774-43	Sequence 43, Appl
19	731	22.9	506	2	US-09-795-926-31	Sequence 31, Appl
20	731	22.9	506	2	US-10-364-774-31	Sequence 31, Appl
21	722.5	22.6	631	2	US-09-795-926-41	Sequence 41, Appl
22	722.5	22.6	631	2	US-10-364-774-41	Sequence 41, Appl
23	709.5	22.2	535	2	US-09-795-926-29	Sequence 29, Appl
24	709.5	22.2	535	2	US-10-364-774-29	Sequence 29, Appl
25	694	21.8	639	2	US-09-376-856-2	Sequence 2, Appli
26	694	21.8	639	2	US-10-012-231A-347	Sequence 347, App
27	694	21.8	639	2	US-10-015-389A-347	Sequence 347, App
28	694	21.8	639	2	US-10-006-768A-347	Sequence 347, App
29	694	21.8	639	2	US-10-015-671A-347	Sequence 347, App
30	694	21.8	639	2	US-10-015-393A-347	Sequence 347, App
31	694	21.8	639	2	US-10-011-833A-347	Sequence 347, App
32	694	21.8	639	2	US-10-006-041A-347	Sequence 347, App
33	694	21.8	639	2	US-10-012-064A-347	Sequence 347, App
34	694	21.8	639	2	US-10-015-392A-347	Sequence 347, App
35	694	21.8	639	3	US-10-011-795B-347	Sequence 347, App
36	694	21.8	639	3	US-10-015-386A-347	Sequence 347, App
37	694	21.8	639	3	US-10-012-121A-347	Sequence 347, App
38	694	21.8	639	3	US-10-006-485A-347	Sequence 347, App
39	694	21.8	639	3	US-10-006-746A-347	Sequence 347, App
40	694	21.8	639	3	US-10-012-752A-347	Sequence 347, App
41	694	21.8	639	3	US-10-017-253A-347	Sequence 347, App
42	694	21.8	639	3	US-10-015-519A-347	Sequence 347, App
43	694	21.8	639	3	US-10-015-715A-347	Sequence 347, App
44	694	21.8	639	3	US-10-007-236A-347	Sequence 347, App
45	688	21.6	638	2	US-09-347-488-2	Sequence 2, Appli

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OM protein - protein search, using sw model

Run on: August 16, 2006, 00:51:25 ; Search time 183 Seconds
 (without alignments)
 1526.331 Million cell updates/sec

Title: US-10-713-345-2
 Perfect score: 3190
 Sequence: 1 MAVARKIRTLLTVNILVFGV.....VQRCSGQKWMIRNWKHARH 603

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA_Main:*
 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	3190	100.0	603	3	US-09-973-457-2
2	3190	100.0	603	4	US-10-369-022-16
3	3190	100.0	603	4	US-10-184-648-43
4	3190	100.0	603	4	US-10-713-345-2
5	2052.5	64.3	598	4	US-10-060-895A-3
6	2052.5	64.3	598	5	US-10-467-903-10
7	1732	54.3	468	4	US-10-210-130-42
8	1732	54.3	468	5	US-10-635-398-62
9	1732	54.3	468	5	US-10-635-398-68
10	1732	54.3	468	5	US-10-635-398-70
11	1731	54.3	468	5	US-10-635-398-66
12	1625	50.9	435	5	US-10-635-398-64
13	1586	49.7	607	4	US-10-288-252-17
14	1586	49.7	607	4	US-10-094-749-1876
15	1586	49.7	607	4	US-10-398-038-17
16	1586	49.7	607	5	US-10-976-440-17
17	1571	49.2	607	4	US-10-210-130-48
18	1571	49.2	607	4	US-10-210-130-50
19	1571	49.2	607	4	US-10-210-130-52
20	1474	46.2	354	4	US-10-094-749-1755
21	1085	34.0	297	4	US-10-104-047-2441
22	1085	34.0	297	6	US-11-072-512-2441
23	1077	33.8	297	4	US-10-108-260A-2888
24	949	29.7	177	4	US-10-292-896-116
25	949	29.7	177	5	US-10-705-401-11
26	949	29.7	177	5	US-10-705-401-113
27	931.5	29.2	556	4	US-10-292-896-62
28	931.5	29.2	556	5	US-10-467-903-9
29	931.5	29.2	556	5	US-10-705-401-59
30	924.5	29.0	273	3	US-09-833-245-1382
31	924.5	29.0	273	6	US-11-264-096-1382
32	906.5	28.4	559	4	US-10-001-851-23
33	906.5	28.4	559	6	US-11-120-749-23
34	901.5	28.3	559	4	US-10-001-851-22
35	901.5	28.3	559	4	US-10-001-851-24
36	901.5	28.3	559	6	US-11-120-749-22
37	901.5	28.3	559	6	US-11-120-749-24
38	899.5	28.2	559	5	US-10-287-436A-554
39	899.5	28.2	559	5	US-10-287-436A-1245
40	899.5	28.2	561	3	US-09-925-301-1006
41	895.5	28.1	559	4	US-10-001-851-20
42	895.5	28.1	559	5	US-10-756-149-4968
43	895.5	28.1	559	6	US-11-120-749-20
44	892.5	28.0	559	4	US-10-001-851-21
45	892.5	28.0	559	4	US-10-205-219-36

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: August 16, 2006, 00:59:40 ; Search time 35 Seconds
 (without alignments)
 1159.690 Million cell updates/sec

Title: US-10-713-345-2
 Perfect score: 3190
 Sequence: 1 MAVARKIRTLLTVNILVFVG.....VQRCSGQKWMIRNWIHARH 603

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA_New:*
 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3190	100.0	603	7	US-11-312-958-16	Sequence 16, Appl
2	1077	33.8	297	7	US-11-293-697-2888	Sequence 2888, Ap
3	895.5	28.1	559	7	US-11-221-332-110	Sequence 110, App
4	694	21.8	639	6	US-10-196-749-364	Sequence 364, App
5	471	14.8	372	7	US-11-293-697-2779	Sequence 2779, Ap
6	154	4.8	28	7	US-11-134-871-1175	Sequence 1175, Ap
7	115.5	3.6	301	6	US-10-734-719-27	Sequence 27, Appl
8	113	3.5	303	6	US-10-734-719-29	Sequence 29, Appl
9	109.5	3.4	646	7	US-11-021-837-58	Sequence 58, Appl
10	106	3.3	702	7	US-11-178-560-1	Sequence 1, Appli
11	106	3.3	703	7	US-11-253-453-11	Sequence 11, Appl
12	106	3.3	972	7	US-11-253-453-1	Sequence 1, Appli
13	106	3.3	972	7	US-11-233-089-52	Sequence 52, Appl
14	101	3.2	297	6	US-10-734-719-31	Sequence 31, Appl
15	96.5	3.0	387	6	US-10-953-349-19574	Sequence 19574, A
16	96.5	3.0	387	7	US-11-056-355B-54283	Sequence 54283, A
17	96	3.0	397	6	US-10-449-902-33856	Sequence 33856, A
18	96	3.0	397	6	US-10-449-902-44582	Sequence 44582, A
19	96	3.0	512	7	US-11-056-355B-10071	Sequence 10071, A
20	95	3.0	420	7	US-11-121-154-139	Sequence 139, App
21	92.5	2.9	709	7	US-11-056-355B-48099	Sequence 48099, A
22	92	2.9	329	6	US-10-953-349-5461	Sequence 5461, Ap
23	91.5	2.9	400	7	US-11-056-355B-47639	Sequence 47639, A
24	90.5	2.8	2413	6	US-10-511-937-2616	Sequence 2616, Ap
25	90	2.8	468	6	US-10-953-349-10909	Sequence 10909, A
26	90	2.8	468	7	US-11-056-355B-20507	Sequence 20507, A
27	90	2.8	469	6	US-10-953-349-10908	Sequence 10908, A
28	90	2.8	469	7	US-11-056-355B-20506	Sequence 20506, A
29	90	2.8	503	6	US-10-953-349-10907	Sequence 10907, A
30	90	2.8	503	7	US-11-056-355B-20505	Sequence 20505, A
31	90	2.8	668	7	US-11-056-355B-45266	Sequence 45266, A
32	90	2.8	707	7	US-11-056-355B-45265	Sequence 45265, A
33	90	2.8	1057	6	US-10-539-228-799	Sequence 799, App
34	89.5	2.8	270	6	US-10-734-719-39	Sequence 39, Appl
35	89.5	2.8	415	7	US-11-056-355B-38748	Sequence 38748, A
36	89.5	2.8	415	7	US-11-056-355B-44051	Sequence 44051, A
37	89.5	2.8	415	7	US-11-056-355B-78318	Sequence 78318, A
38	89.5	2.8	415	7	US-11-056-355B-98701	Sequence 98701, A
39	89.5	2.8	415	7	US-11-056-355B-109940	Sequence 109940, A
40	89.5	2.8	416	7	US-11-056-355B-38747	Sequence 38747, A
41	89.5	2.8	416	7	US-11-056-355B-44050	Sequence 44050, A
42	89.5	2.8	416	7	US-11-056-355B-78317	Sequence 78317, A
43	89.5	2.8	416	7	US-11-056-355B-98700	Sequence 98700, A
44	89.5	2.8	416	7	US-11-056-355B-109939	Sequence 109939, A

45 89.5 2.8 450 7 US-11-056-355B-38746 Sequence 38746, A

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: August 16, 2006, 00:41:10 ; Search time 43 Seconds
(without alignments)
1349.272 Million cell updates/sec

Title: US-10-713-345-2
Perfect score: 3190
Sequence: 1 MAVARKIRTLLTVNILVFGV.....VQRCSGQKWMIRNWKHARH 603

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	906.5	28.4	559	2	A45987	polypeptide N-acet
2	899.5	28.2	559	2	JC4223	polypeptide N-acet
3	878	27.5	612	2	T42243	probable polypepti
4	869	27.2	563	2	A88515	polypeptide N-acet
5	868.5	27.2	624	2	T42247	polypeptide N-acet
6	866.5	27.2	626	2	T42246	polypeptide N-acet
7	857	26.9	623	2	T42245	probable polypepti
8	796	25.0	589	2	T42244	probable polypepti
9	794.5	24.9	571	2	I37405	polypeptide N-acet
10	782	24.5	601	2	T42251	polypeptide N-acet
11	761.5	23.9	618	2	T42248	polypeptide N-acet
12	761	23.9	617	2	T42249	polypeptide N-acet
13	745.5	23.4	579	2	T31549	polypeptide N-acet
14	744	23.3	633	2	JC5247	polypeptide N-acet
15	738.5	23.2	562	2	T42250	polypeptide N-acet
16	735	23.0	605	2	T27397	hypothetical prote
17	735	23.0	684	2	T26930	hypothetical prote
18	610.5	19.1	421	2	T42252	polypeptide N-acet
19	362	11.3	133	2	T46260	hypothetical prote
20	220.5	6.9	276	2	T12552	hypothetical prote
21	151.5	4.7	470	2	C70641	hypothetical prote
22	147.5	4.6	324	2	A69290	probable glycosyl
23	134.5	4.2	525	2	A45053	proteinase RPI - R
24	126.5	4.0	302	2	A84263	hypothetical prote
25	119.5	3.7	697	2	JN0602	rfb protein - Esch
26	118	3.7	1405	1	S13421	polymeric globin a
27	117	3.7	726	2	A47275	transferrin - cock
28	117	3.7	1275	2	T18556	O-antigen biosynth
29	113.5	3.6	1044	2	H97186	glycosyltransferas
30	113	3.5	303	2	F81318	probable galactosy
31	112	3.5	324	2	AB2190	hypothetical prote
32	107.5	3.4	439	2	AF2602	nicotinate phospho
33	107.5	3.4	439	2	F97384	nicotinate phospho
34	107	3.4	313	2	AI2202	hypothetical prote
35	107	3.4	377	2	JC7535	chitinase (EC 3.2.
36	106	3.3	972	2	T09595	glucuronosyltransf
37	105	3.3	328	2	B84263	succinoglycan bios
38	104	3.3	348	2	T13320	hypothetical prote
39	104	3.3	503	2	B84007	cardiolipin synthe
40	103.5	3.2	362	2	G75191	dolichol-phosphate
41	103	3.2	348	2	T13625	hypothetical prote
42	103	3.2	685	2	AH3414	soluble lytic mure
43	101	3.2	293	2	AB3124	glycosyltransferas
44	101	3.2	293	2	G98163	dtbP-rha, A-D-glc
45	101	3.2	787	2	H98163	hypothetical prote

43	931.5	29.2	556	9	ADX58181	Adx58181 Human pol
44	931.5	29.2	556	10	AEF65468	Aef65468 Human GAL
45	931.5	29.2	557	7	ADB76895	Adb76895 Human N-a

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OM protein - protein search, using sw model

Run on: August 16, 2006, 00:37:44 ; Search time 303 Seconds
(without alignments)
1840.873 Million cell updates/sec

Title: US-10-713-345-2
Perfect score: 3190
Sequence: 1 MAVARKIRTLLTVNIIIVFVG.....VQRCSGQKWMIRNWIKHARH 603

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3179	99.7	603	1	GALT9_HUMAN	Q9hcg5 h polypepti
2	2876.5	90.2	606	1	GALT9_MACFA	Q9gm01 m polypepti
3	2052.5	64.3	598	1	GLTL3_HUMAN	Q6is24 h putative
4	2052.5	64.3	598	2	Q2L4S5_HUMAN	Q2L4s5 homo sapien
5	2051.5	64.3	598	1	GLTL3_MOUSE	Q7tt15 m putative
6	2051.5	64.3	598	2	Q59J92_MOUSE	Q59j92 mus musculu
7	2047.5	64.2	598	2	Q58A53_HUMAN	Q58a53 homo sapien
8	2047.5	64.2	598	2	Q5CD99_RAT	Q5cd99 rattus norv
9	1929	60.5	611	2	Q4RFU6_TETNG	Q4rfu6 tetraodon n
10	1757.5	55.1	554	2	Q4RPK0_TETNG	Q4rpk0 tetraodon n
11	1586	49.7	607	2	Q58A54_HUMAN	Q58a54 homo sapien
12	1584	49.7	607	2	Q59J91_MOUSE	Q59j91 mus musculu
13	1581	49.6	607	1	GLTL4_HUMAN	Q6p9a2 h putative
14	1566.5	49.1	622	1	GLTL4_MOUSE	Q8klb9 m putative
15	1390.5	43.6	534	2	Q4SVX6_TETNG	Q4svx6 tetraodon n
16	1328	41.6	266	2	Q52LR8_HUMAN	Q52lr8 homo sapien
17	1319	41.3	637	1	GALT8_HUMAN	Q9ny28 h probable
18	1243	39.0	237	2	Q3TB05_MOUSE	Q3tb05 mus musculu
19	1230.5	38.6	462	2	Q5RI00_BRARE	Q5ri00 brachydanio
20	1166	36.6	423	2	Q5RHZ9_BRARE	Q5rhz9 brachydanio
21	1085.5	34.0	530	2	Q4SKF7_TETNG	Q4skf7 tetraodon n
22	949	29.7	177	2	Q68VJ2_HUMAN	Q68vj2 homo sapien
23	932.5	29.2	556	1	GLT13_MOUSE	Q8cf93 m polypepti
24	932.5	29.2	556	1	GLT13_RAT	Q6ue39 r polypepti
25	931.5	29.2	556	1	GLT13_HUMAN	Q8iuc8 h polypepti
26	931.5	29.2	556	2	Q68VI8_HUMAN	Q68vi8 homo sapien
27	931.5	29.2	556	2	Q6GM51_XENLA	Q6gm51 xenopus lae
28	910.5	28.5	559	2	Q5ZJL1_CHICK	Q5zjl1 gallus gall
29	906.5	28.4	559	1	GALT1_BOVIN	Q07537 b polypepti
30	901.5	28.3	559	1	GALT1_MOUSE	Q08912 m polypepti
31	901.5	28.3	559	1	GALT1_PIG	Q29121 s polypepti
32	901.5	28.3	559	2	Q5BKS3_MOUSE	Q5bks3 mus musculu
33	899.5	28.2	559	1	GALT1_HUMAN	Q10472 h polypepti
34	893.5	28.0	559	2	Q6PA81_XENLA	Q6pa81 xenopus lae
35	892.5	28.0	559	1	GALT1_RAT	Q10473 r polypepti
36	878	27.5	612	1	GALT3_CAEEL	P34678 caenorhabdi
37	875.5	27.4	611	2	Q61DZ1_CAEEL	Q61dz1 caenorhabdi
38	871	27.3	630	1	GALT5_DROME	Q6wv17 drosophila
39	862.5	27.0	626	1	GALT5_CAEEL	Q95zjl caenorhabdi
40	862	27.0	404	2	Q4SIA0_TETNG	Q4sia0 tetraodon n
41	862	27.0	632	2	Q4RQL8_TETNG	Q4rql8 tetraodon n
42	861	27.0	603	2	Q68F39_XENLA	Q68f39 xenopus lae
43	858	26.9	563	2	Q6DJR8_XENTR	Q6djr8 xenopus tro
44	853	26.7	578	1	GALT4_HUMAN	Q8n4a0 h polypepti
45	853	26.7	608	1	GLT11_MOUSE	Q92118 m polypepti

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 00:45:58 ; Search time 14669.9 Seconds
 (without alignments)
 11211.577 Million cell updates/sec

Title: US-10-713-345-1
 Perfect score: 2572
 Sequence: 1 gcgccgccccgccgcgcctt.....ccccagcacttgcggccgc 2572

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : GenEmbl:*
 1: gb_env:*
 2: gb_pat:*
 3: gb_ph:*
 4: gb_pl:*
 5: gb_pr:*
 6: gb_ro:*
 7: gb_sts:*
 8: gb_sy:*
 9: gb_un:*
 10: gb_vi:*
 11: gb_ov:*
 12: gb_htg:*
 13: gb_in:*
 14: gb_om:*
 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2572	100.0	2572	2	AR483255	AR483255 Sequence
2	2006.2	78.0	2183	5	AK055773	AK055773 Homo sapi
3	1980	77.0	2535	5	AB050509	AB050509 Macaca fa
4	1812	70.5	1812	2	AR483256	AR483256 Sequence
5	1805.6	70.2	1812	5	AB040672	AB040672 Homo sapi
6	1171.4	45.5	1727	2	AX713432	AX713432 Sequence
7	1171.4	45.5	1727	5	AK054820	AK054820 Homo sapi
8	1171	45.5	1742	5	AF458594	AF458594 Homo sapi
9	786.6	30.6	3439	2	AX574388	AX574388 Sequence
10	784.8	30.5	3333	2	AX544488	AX544488 Sequence
11	783.4	30.5	1797	2	AX544489	AX544489 Sequence
12	783.4	30.5	1797	5	AJ626726	AJ626726 Homo sapi
13	783.4	30.5	1945	5	BC069624	BC069624 Homo sapi
14	783.4	30.5	1945	5	BC069628	BC069628 Homo sapi
15	783.4	30.5	1945	5	BC069636	BC069636 Homo sapi
16	783.4	30.5	3298	5	AF410457	AF410457 Homo sapi
17	781.8	30.4	1945	5	BC069645	BC069645 Homo sapi
18	781.8	30.4	1994	5	BC067524	BC067524 Homo sapi
19	781.8	30.4	1994	5	BC067525	BC067525 Homo sapi
20	781.8	30.4	1994	5	BC069997	BC069997 Homo sapi
21	778.6	30.3	1797	5	AB078148	AB078148 Homo sapi
22	771.4	30.0	1797	6	AB040671	AB040671 Rattus no
23	769	29.9	836	5	BC093817	BC093817 Homo sapi
24	769	29.9	836	5	BC093819	BC093819 Homo sapi
25	756.8	29.4	3580	6	BC052469	BC052469 Mus muscu
26	756.8	29.4	4132	6	BC069177	BC069177 Mus muscu
27	755.4	29.4	1797	6	AB175684	AB175684 Mus muscu
28	748.4	29.1	3653	2	CQ843080	CQ843080 Sequence
29	748.4	29.1	3653	5	AK126044	AK126044 Homo sapi
30	744.2	28.9	3183	2	CS167200	CS167200 Sequence
31	744.2	28.9	3183	2	AX833321	AX833321 Sequence
32	744.2	28.9	3183	5	AK094958	AK094958 Homo sapi
33	738	28.7	2278	6	AF467979	AF467979 Mus muscu
34	658	25.6	658	2	CQ724811	CQ724811 Sequence
c 35	589.2	22.9	664	5	HSA339305	AJ339305 Homo sapi
c 36	589.2	22.9	129492	5	AC138466	AC138466 Homo sapi
37	588	22.9	2496	2	AX713553	AX713553 Sequence

38	588	22.9	2496	5	AK055111	AK055111 Homo sapi
39	588	22.9	2519	5	BC060864	BC060864 Homo sapi
40	588	22.9	2520	5	BC037341	BC037341 Homo sapi
41	588	22.9	2534	2	AX451430	AX451430 Sequence
42	587.2	22.8	1824	6	AB175685	AB175685 Mus muscu
43	586.6	22.8	1824	5	AB078147	AB078147 Homo sapi
44	586.6	22.8	1824	5	AJ626724	AJ626724 Homo sapi
45	579.2	22.5	1981	5	AB050513	AB050513 Macaca fa

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 00:44:33 ; Search time 1619.23 Seconds
 (without alignments)
 11074.760 Million cell updates/sec

Title: US-10-713-345-1
 Perfect score: 2572
 Sequence: 1 gcgccgccccgccgcctt.....ccccagcacttgcggccgc 2572

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_8:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*
 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2572	100.0	2572	8	ABX14500	Abx14500 cDNA enco
2	2572	100.0	2572	10	ADC77652	Adc77652 Human 471
3	2572	100.0	2572	12	ADM46165	Adm46165 cDNA enco
4	2241.6	87.2	2410	12	ADQ24697	Adq24697 Human sof
5	1812	70.5	1812	12	ADM46167	Adm46167 ORF of cD
6	1386.4	53.9	1525	4	AAI59554	Aai59554 Human pol
7	1171.4	45.5	1727	10	ADA52548	Ada52548 Human cod
8	1131.6	44.0	1322	5	ABA11363	Abal1363 Human ner
9	952.8	37.0	956	4	AAI61340	Aai61340 Human pol
10	797.4	31.0	799	3	AAC75948	Aac75948 Human ORF
11	786.6	30.6	3439	6	ABK91321	Abk91321 cDNA enco
12	784.8	30.5	3333	6	ABV85011	Abv85011 Human pp-
13	783.4	30.5	1797	6	ABV85012	Abv85012 Human pp-
14	778.6	30.3	1797	10	ADC35397	Adc35397 Human N-a
15	778.4	30.3	2557	13	ADS10210	Ads10210 Human the
16	773.8	30.1	1915	4	AAI60831	Aai60831 Human pol
17	748.4	29.1	3653	12	ADQ64566	Adq64566 Novel hum
18	744.2	28.9	3183	11	ADM01760	Adm01760 Human cDN
19	744.2	28.9	3183	14	AEC84690	Aec84690 Human cDN
20	689.4	26.8	3109	10	ADE47679	Ade47679 Human NOV
21	689.4	26.8	3109	12	ADJ78949	Adj78949 Human NOV
22	689.4	26.8	3109	12	ADJ71668	Adj71668 Human NOV
23	689.4	26.8	3109	12	ADJ71660	Adj71660 Human NOV
24	689.4	26.8	3109	12	ADJ71666	Adj71666 Human NOV
25	687.8	26.7	3109	12	ADJ71664	Adj71664 Human NOV
26	639.8	24.9	1306	12	ADJ71662	Adj71662 Human NOV
27	634.4	24.7	982	5	ABA11032	Abal1032 Human ner
28	588	22.9	2496	10	ADA52669	Ada52669 Human cod
29	588	22.9	2519	9	ACH04034	Ach04034 Human cDN
30	588	22.9	2534	6	AAD35232	Aad35232 Human TRN
31	586.6	22.8	1824	10	ADC35396	Adc35396 Human N-a
32	584.8	22.7	2422	10	ADE47689	Ade47689 Human NOV
33	584.8	22.7	2422	10	ADE47687	Ade47687 Human NOV
34	584.8	22.7	2422	10	ADE47685	Ade47685 Human NOV
35	584.8	22.7	2422	12	ADJ78957	Adj78957 Human NOV
36	584.8	22.7	2422	12	ADJ78955	Adj78955 Human NOV
37	584.8	22.7	2422	12	ADJ78959	Adj78959 Human NOV

	38	532.4	20.7	534	10	ADE25971	Ade25971 N-acetyl
	39	532.4	20.7	534	14	ADX58234	Adx58234 Human pol
c	40	505	19.6	505	12	ADQ20725	Adq20725 Human sof
	41	476.2	18.5	2465	10	ADB62317	Adb62317 Human cDN
	42	424.4	16.5	2388	4	AAI60021	Aai60021 Human pol
	43	424.4	16.5	2388	13	ADS11539	Ads11539 Human the
	44	422.8	16.4	2416	4	AAI58235	Aai58235 Human pol
	45	422.8	16.4	2416	5	ADQ98442	Adq98442 DNA encod

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 01:13:47 ; Search time 480.49 Seconds
 (without alignments)
 10015.801 Million cell updates/sec

Title: US-10-713-345-1
 Perfect score: 2572
 Sequence: 1 gcgcgcgcgcgcgcgcctt.....ccccagcacttgcggccgc 2572

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents_NA:*
 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2572	100.0	2572	3	US-09-973-457-1	Sequence 1, Appli
2	1812	70.5	1812	3	US-09-973-457-3	Sequence 3, Appli
3	1171.4	45.5	1727	4	US-10-094-749-116	Sequence 116, App
4	588	22.9	2496	4	US-10-094-749-237	Sequence 237, App
5	476.2	18.5	2465	3	US-10-104-047-471	Sequence 471, App
6	422.8	16.4	2416	3	US-09-620-312D-112	Sequence 112, App
7	368	14.3	903	3	US-09-620-312D-938	Sequence 938, App
8	222.4	8.6	2199	3	US-09-799-451-328	Sequence 328, App
9	208.4	8.1	1540	3	US-09-270-767-11959	Sequence 11959, A
10	204.2	7.9	1920	3	US-09-376-856-1	Sequence 1, Appli
11	204.2	7.9	2575	3	US-10-012-231A-346	Sequence 346, App
12	204.2	7.9	2575	3	US-10-015-389A-346	Sequence 346, App
13	204.2	7.9	2575	3	US-10-006-768A-346	Sequence 346, App
14	204.2	7.9	2575	3	US-10-015-671A-346	Sequence 346, App
15	204.2	7.9	2575	3	US-10-015-393A-346	Sequence 346, App
16	204.2	7.9	2575	3	US-10-011-833A-346	Sequence 346, App
17	204.2	7.9	2575	3	US-10-006-041A-346	Sequence 346, App
18	204.2	7.9	2575	3	US-10-012-064A-346	Sequence 346, App
19	204.2	7.9	2575	4	US-10-015-392A-346	Sequence 346, App
20	204.2	7.9	2575	5	US-10-011-795B-346	Sequence 346, App
21	204.2	7.9	2575	5	US-10-015-386A-346	Sequence 346, App
22	204.2	7.9	2575	5	US-10-012-121A-346	Sequence 346, App
23	204.2	7.9	2575	5	US-10-006-485A-346	Sequence 346, App
24	204.2	7.9	2575	5	US-10-006-746A-346	Sequence 346, App
25	204.2	7.9	2575	5	US-10-012-752A-346	Sequence 346, App
26	204.2	7.9	2575	5	US-10-017-253A-346	Sequence 346, App
27	204.2	7.9	2575	5	US-10-015-519A-346	Sequence 346, App
28	204.2	7.9	2575	5	US-10-015-715A-346	Sequence 346, App
29	204.2	7.9	2575	5	US-10-007-236A-346	Sequence 346, App
30	203.2	7.9	2095	3	US-10-104-047-435	Sequence 435, App
31	202.6	7.9	3332	3	US-09-347-488-1	Sequence 1, Appli
32	190	7.4	740	3	US-09-270-767-27636	Sequence 27636, A
33	186.4	7.2	1521	3	US-09-795-926-30	Sequence 30, Appl
34	186.4	7.2	1521	3	US-10-364-774-30	Sequence 30, Appl
35	186.4	7.2	1812	3	US-09-795-926-42	Sequence 42, Appl
36	186.4	7.2	1812	3	US-10-364-774-42	Sequence 42, Appl
37	186.4	7.2	3896	3	US-09-795-926-44	Sequence 44, Appl
38	186.4	7.2	3896	3	US-10-364-774-44	Sequence 44, Appl
39	171.6	6.7	1746	3	US-10-074-527-3	Sequence 3, Appli
40	171.6	6.7	2850	3	US-10-074-527-1	Sequence 1, Appli
c 41	154.6	6.0	910	3	US-09-270-767-2104	Sequence 2104, Ap
c 42	154.6	6.0	910	3	US-09-270-767-17386	Sequence 17386, A

c	43	144.4	5.6	868	3	US-09-270-767-13764	Sequence 13764, A
	44	137.4	5.3	1771	3	US-09-976-594-28	Sequence 28, Appl
	45	133.2	5.2	810	3	US-09-795-926-26	Sequence 26, Appl

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 01:42:59 ; Search time 4212.94 Seconds
(without alignments)
7501.600 Million cell updates/sec

Title: US-10-713-345-1
Perfect score: 2572
Sequence: 1 gcgcgcgcgcgcgcgcctt.....ccccagcacttgcgcgcgc 2572

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2572	100.0	2572	3	US-09-973-457-1	Sequence 1, Appli
2	2572	100.0	2572	7	US-10-369-022-15	Sequence 15, Appl
3	2572	100.0	2572	7	US-10-184-648-42	Sequence 42, Appl
4	2572	100.0	2572	8	US-10-713-345-1	Sequence 1, Appli
5	2241.6	87.2	2410	9	US-10-723-860-7517	Sequence 7517, Ap
6	1812	70.5	1812	3	US-09-973-457-3	Sequence 3, Appli
7	1812	70.5	1812	7	US-10-184-648-44	Sequence 44, Appl
8	1812	70.5	1812	8	US-10-713-345-3	Sequence 3, Appli
9	1171.4	45.5	1727	7	US-10-094-749-116	Sequence 116, App
10	786.6	30.6	3439	9	US-10-467-903-21	Sequence 21, Appl
11	784.8	30.5	3333	6	US-10-060-895A-1	Sequence 1, Appli
12	783.4	30.5	1797	6	US-10-060-895A-2	Sequence 2, Appli
13	744.2	28.9	3183	7	US-10-108-260A-445	Sequence 445, App
14	689.4	26.8	3109	8	US-10-210-130-41	Sequence 41, Appl
15	689.4	26.8	3109	9	US-10-635-398-61	Sequence 61, Appl
16	689.4	26.8	3109	9	US-10-635-398-67	Sequence 67, Appl
17	689.4	26.8	3109	9	US-10-635-398-69	Sequence 69, Appl
18	687.8	26.7	3109	9	US-10-635-398-65	Sequence 65, Appl
19	639.8	24.9	1306	9	US-10-635-398-63	Sequence 63, Appl
20	588	22.9	2496	7	US-10-094-749-237	Sequence 237, App
21	588	22.9	2519	6	US-10-116-802-239	Sequence 239, App
22	588	22.9	2534	7	US-10-288-252-37	Sequence 37, Appl
23	588	22.9	2534	8	US-10-398-038-37	Sequence 37, Appl
24	588	22.9	2534	10	US-10-976-440-37	Sequence 37, Appl
25	584.8	22.7	2422	8	US-10-210-130-47	Sequence 47, Appl
26	584.8	22.7	2422	8	US-10-210-130-49	Sequence 49, Appl
27	584.8	22.7	2422	8	US-10-210-130-51	Sequence 51, Appl
28	532.4	20.7	534	7	US-10-292-896-115	Sequence 115, App
29	532.4	20.7	534	9	US-10-705-401-112	Sequence 112, App
c 30	505	19.6	505	9	US-10-723-860-3545	Sequence 3545, Ap
31	476.2	18.5	2465	7	US-10-104-047-471	Sequence 471, App
32	476.2	18.5	2465	16	US-11-072-512-471	Sequence 471, App
33	422.8	16.4	2416	6	US-10-037-270-112	Sequence 112, App
34	422.8	16.4	2416	7	US-10-117-722-112	Sequence 112, App
35	422.8	16.4	2416	10	US-10-122-851-112	Sequence 112, App
36	402.2	15.6	453	3	US-09-918-995-28101	Sequence 28101, A

37	368	14.3	903	6	US-10-037-270-938	Sequence 938, App
38	368	14.3	903	7	US-10-117-722-938	Sequence 938, App
39	368	14.3	903	10	US-10-122-851-938	Sequence 938, App
40	354.4	13.8	1271	8	US-10-276-723-1	Sequence 1, Appli
41	334.8	13.0	580	8	US-10-210-130-43	Sequence 43, Appl
42	293.4	11.4	793	6	US-10-060-895A-4	Sequence 4, Appli
43	292	11.4	757	6	US-10-060-895A-6	Sequence 6, Appli
44	235.6	9.2	1869	9	US-10-789-241-47	Sequence 47, Appl
45	235.6	9.2	1869	10	US-10-756-149-1870	Sequence 1870, Ap

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 01:59:47 ; Search time 451.156 Seconds
(without alignments)
9113.283 Million cell updates/sec

Title: US-10-713-345-1
Perfect score: 2572
Sequence: 1 gcgcgcgcgcgcgcgcctt.....ccccagcacttgcgcgcgc 2572

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
1	2572	100.0	2572	8	US-11-312-958-15	Sequence 15, Appl
2	783.4	30.5	3298	8	US-11-266-748A-56451	Sequence 56451, A
3	744.2	28.9	3183	8	US-11-293-697-445	Sequence 445, App
4	588	22.9	2519	8	US-11-266-748A-31678	Sequence 31678, A
5	588	22.9	2519	8	US-11-266-748A-56113	Sequence 56113, A
6	454	17.7	794	8	US-11-266-748A-1713	Sequence 1713, Ap
7	370	14.4	2135	8	US-11-266-748A-23941	Sequence 23941, A
8	370	14.4	2135	8	US-11-266-748A-57086	Sequence 57086, A
9	316.2	12.3	920	8	US-11-266-748A-190028	Sequence 190028,
10	238.2	9.3	1000	8	US-11-266-748A-406202	Sequence 406202,
c 11	238.2	9.3	1000	8	US-11-266-748A-477248	Sequence 477248,
c 12	235.6	9.2	2332	8	US-11-266-748A-189071	Sequence 189071,
13	235.6	9.2	2332	8	US-11-266-748A-242737	Sequence 242737,
14	235.6	9.2	2819	8	US-11-266-748A-27039	Sequence 27039, A
15	204.2	7.9	2575	6	US-10-196-749-363	Sequence 363, App
16	204.2	7.9	3580	8	US-11-266-748A-56877	Sequence 56877, A
17	186.4	7.2	5222	8	US-11-266-748A-31657	Sequence 31657, A
18	184.4	7.2	3105	8	US-11-293-697-336	Sequence 336, App
19	173.8	6.8	1163	8	US-11-266-748A-367663	Sequence 367663,
c 20	173.8	6.8	1163	8	US-11-266-748A-451042	Sequence 451042,
21	170	6.6	1746	8	US-11-266-748A-22604	Sequence 22604, A
22	165.4	6.4	1542	8	US-11-266-748A-188164	Sequence 188164,
23	165.4	6.4	4464	8	US-11-266-748A-27336	Sequence 27336, A
24	164.4	6.4	650	7	US-11-190-172-4285	Sequence 4285, Ap
25	151.8	5.9	1140	8	US-11-266-748A-96859	Sequence 96859, A
c 26	151.8	5.9	1140	8	US-11-266-748A-149670	Sequence 149670,
27	135.4	5.3	5360	8	US-11-266-748A-57295	Sequence 57295, A
28	131.4	5.1	1635	8	US-11-266-748A-183850	Sequence 183850,
c 29	128.4	5.0	968	8	US-11-266-748A-370880	Sequence 370880,
30	128.4	5.0	968	8	US-11-266-748A-454259	Sequence 454259,
31	119.8	4.7	2185	8	US-11-221-332-109	Sequence 109, App
32	117	4.5	818	8	US-11-266-748A-356278	Sequence 356278,
33	117	4.5	818	8	US-11-266-748A-385814	Sequence 385814,
c 34	117	4.5	818	8	US-11-266-748A-439657	Sequence 439657,
c 35	111	4.3	769	8	US-11-266-748A-259798	Sequence 259798,
c 36	111	4.3	769	8	US-11-266-748A-279021	Sequence 279021,
37	111	4.3	769	8	US-11-266-748A-320315	Sequence 320315,
38	104	4.0	1000	8	US-11-266-748A-399106	Sequence 399106,
c 39	104	4.0	1000	8	US-11-266-748A-470152	Sequence 470152,
40	103.8	4.0	1066	8	US-11-266-748A-360857	Sequence 360857,
c 41	103.8	4.0	1066	8	US-11-266-748A-444236	Sequence 444236,
42	103	4.0	862	8	US-11-266-748A-98276	Sequence 98276, A

c	43	103	4.0	862	8	US-11-266-748A-151087	Sequence 151087,
	44	96.4	3.7	869	8	US-11-266-748A-98384	Sequence 98384, A
c	45	96.4	3.7	869	8	US-11-266-748A-151195	Sequence 151195,

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 00:50:04 ; Search time 12286.2 Seconds
 (without alignments)
 11706.157 Million cell updates/sec

Title: US-10-713-345-1
 Perfect score: 2572
 Sequence: 1 gcgccgccccgccgcgcctt.....ccccagcacttgcggccgc 2572

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*
 1: gb_est1:*
 2: gb_est3:*
 3: gb_est4:*
 4: gb_est5:*
 5: gb_est6:*
 6: gb_htc:*
 7: gb_est2:*
 8: gb_est7:*
 9: gb_est8:*
 10: gb_est9:*
 11: gb_gss1:*
 12: gb_gss2:*
 13: gb_gss3:*
 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1418	55.1	2886	6	AK032568	AK032568 Mus muscu
2	1180.8	45.9	1368	14	DQ048170	DQ048170 Homo sapi
3	838.8	32.6	1056	3	BM925654	BM925654 AGENCOURT
4	813.2	31.6	1322	14	DQ048171	DQ048171 Pan trogl
5	783.4	30.5	1797	14	AY407808	AY407808 Homo sapi
6	755.4	29.4	1797	14	AY407810	AY407810 Mus muscu
7	732	28.5	879	2	BI756878	BI756878 603029069
8	720.4	28.0	866	10	DV913368	DV913368 LB02827.C
9	717.6	27.9	1120	3	BM907000	BM907000 AGENCOURT
10	702	27.3	761	2	BI822362	BI822362 603037922
11	678.6	26.4	806	8	CO886915	CO886915 BovGen_15
12	675.6	26.3	839	5	CJ470325	CJ470325 CJ470325
13	655	25.5	655	4	BX099049	BX099049 BX099049
14	645	25.1	1016	10	DV011836	DV011836 CNB271-C0
15	620.8	24.1	624	4	CB152086	CB152086 K-EST0209
16	616.8	24.0	782	8	CN823582	CN823582 Oa_splbn_
17	611.8	23.8	2031	6	AK048758	AK048758 Mus muscu
18	604.8	23.5	652	5	CD630910	CD630910 56006229J
19	602.4	23.4	1797	14	AY407809	AY407809 Pan trogl
20	598.2	23.3	793	2	BI552481	BI552481 603196186
21	595.2	23.1	1990	6	AK035817	AK035817 Mus muscu
22	592.4	23.0	2617	6	AK051281	AK051281 Mus muscu
23	591.8	23.0	1541	6	AK171529	AK171529 Mus muscu
24	588.4	22.9	596	9	DR001000	DR001000 TC112896
25	588	22.9	588	9	DA406079	DA406079 DA406079
26	582.4	22.6	596	9	DA586340	DA586340 DA586340
27	580	22.6	580	9	DA064328	DA064328 DA064328
28	574.4	22.3	576	9	DA079387	DA079387 DA079387
29	574	22.3	574	9	DA086071	DA086071 DA086071
30	568.4	22.1	575	9	DA206384	DA206384 DA206384
31	564	21.9	564	9	DA077079	DA077079 DA077079
32	561	21.8	561	9	DA201413	DA201413 DA201413
33	560.4	21.8	562	9	DA355587	DA355587 DA355587
34	551.4	21.4	553	9	DA122336	DA122336 DA122336
35	549.2	21.4	555	9	DA104563	DA104563 DA104563
36	544.8	21.2	1578	6	AK170381	AK170381 Mus muscu
37	526.2	20.5	531	4	CB154648	CB154648 K-EST0212
38	522.6	20.3	1019	2	BM543465	BM543465 AGENCOURT

39	519	20.2	555	9	DA074160	DA074160	DA074160
40	519	20.2	825	3	BU458046	BU458046	603776544
41	516.6	20.1	1046	10	DW666789	DW666789	CNB338-H1
42	513.4	20.0	525	9	DA624069	DA624069	DA624069
43	512.8	19.9	517	4	CB153078	CB153078	K-EST0210
44	506.4	19.7	780	3	BU385765	BU385765	603861678
c 45	505	19.6	505	7	AW294162	AW294162	UI-H-BI2-

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 00:45:58 ; Search time 10335.1 Seconds
(without alignments)
11211.577 Million cell updates/sec

Title: US-10-713-345-3
Perfect score: 1812
Sequence: 1 atggcgggtggccaggaagat.....tcaaacacgcacgcactga 1812

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1812	100.0	1812	2	AR483256	AR483256 Sequence
2	1812	100.0	2572	2	AR483255	AR483255 Sequence
3	1805.6	99.6	1812	5	AB040672	AB040672 Homo sapi
4	1570.2	86.7	2183	5	AK055773	AK055773 Homo sapi
5	1549.4	85.5	2535	5	AB050509	AB050509 Macaca fa
6	783.4	43.2	1797	2	AX544489	AX544489 Sequence
7	783.4	43.2	1797	5	AJ626726	AJ626726 Homo sapi
8	783.4	43.2	1945	5	BC069624	BC069624 Homo sapi
9	783.4	43.2	1945	5	BC069628	BC069628 Homo sapi
10	783.4	43.2	1945	5	BC069636	BC069636 Homo sapi
11	783.4	43.2	3298	5	AF410457	AF410457 Homo sapi
12	783.4	43.2	3333	2	AX544488	AX544488 Sequence
13	783.4	43.2	3439	2	AX574388	AX574388 Sequence
14	781.8	43.1	1945	5	BC069645	BC069645 Homo sapi
15	781.8	43.1	1994	5	BC067524	BC067524 Homo sapi
16	781.8	43.1	1994	5	BC067525	BC067525 Homo sapi
17	781.8	43.1	1994	5	BC069997	BC069997 Homo sapi
18	778.6	43.0	1797	5	AB078148	AB078148 Homo sapi
19	771.4	42.6	1797	6	AB040671	AB040671 Rattus no
20	755.4	41.7	1797	6	AB175684	AB175684 Mus muscu
21	755.4	41.7	3580	6	BC052469	BC052469 Mus muscu
22	755.4	41.7	4132	6	BC069177	BC069177 Mus muscu
23	748.4	41.3	3653	2	CQ843080	CQ843080 Sequence
24	748.4	41.3	3653	5	AK126044	AK126044 Homo sapi
25	744.2	41.1	3183	2	CS167200	CS167200 Sequence
26	744.2	41.1	3183	2	AX833321	AX833321 Sequence
27	744.2	41.1	3183	5	AK094958	AK094958 Homo sapi
28	736.6	40.7	2278	6	AF467979	AF467979 Mus muscu
29	735.4	40.6	1727	2	AX713432	AX713432 Sequence
30	735.4	40.6	1727	5	AK054820	AK054820 Homo sapi
31	735	40.6	836	5	BC093817	BC093817 Homo sapi
32	735	40.6	836	5	BC093819	BC093819 Homo sapi
33	735	40.6	1742	5	AF458594	AF458594 Homo sapi
34	658	36.3	658	2	CQ724811	CQ724811 Sequence
35	587.2	32.4	1824	6	AB175685	AB175685 Mus muscu
36	586.6	32.4	1824	5	AB078147	AB078147 Homo sapi
37	586.6	32.4	1824	5	AJ626724	AJ626724 Homo sapi

38	586.6	32.4	2496	2	AX713553	AX713553 Sequence
39	586.6	32.4	2496	5	AK055111	AK055111 Homo sapi
40	586.6	32.4	2519	5	BC060864	BC060864 Homo sapi
41	586.6	32.4	2520	5	BC037341	BC037341 Homo sapi
42	586.6	32.4	2534	2	AX451430	AX451430 Sequence
43	579.2	32.0	1981	5	AB050513	AB050513 Macaca fa
44	533.8	29.5	2595	6	BC024988	BC024988 Mus muscu
45	532.4	29.4	534	2	CQ816194	CQ816194 Sequence

GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 00:44:33 ; Search time 1140.77 Seconds
 (without alignments)
 11074.760 Million cell updates/sec

Title: US-10-713-345-3
 Perfect score: 1812
 Sequence: 1 atggcggtggccaggaagat.....tcaaacacgcacggcactga 1812

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_8:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*
 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1812	100.0	1812	12 ADM46167	Adm46167 ORF of cD
2	1812	100.0	2572	8 ABX14500	Abx14500 cDNA enco
3	1812	100.0	2572	10 ADC77652	Adc77652 Human 471
4	1812	100.0	2572	12 ADM46165	Adm46165 cDNA enco
5	1805.6	99.6	2410	12 ADQ24697	Adq24697 Human sof
6	1155.8	63.8	1525	4 AAI59554	Aai59554 Human pol
7	1051.4	58.0	1322	5 ABA11363	Abal1363 Human ner
8	944.8	52.1	956	4 AAI61340	Aai61340 Human pol
9	797.4	44.0	799	3 AAC75948	Aac75948 Human ORF
10	783.4	43.2	1797	6 ABV85012	Abv85012 Human pp-
11	783.4	43.2	3333	6 ABV85011	Abv85011 Human pp-
12	783.4	43.2	3439	6 ABK91321	Abk91321 cDNA enco
13	778.6	43.0	1797	10 ADC35397	Adc35397 Human N-a
14	777.8	42.9	2557	13 ADS10210	Ads10210 Human the
15	773.8	42.7	1915	4 AAI60831	Aai60831 Human pol
16	748.4	41.3	3653	12 ADQ64566	Adq64566 Novel hum
17	744.2	41.1	3183	11 ADM01760	Adm01760 Human cDN
18	744.2	41.1	3183	14 AEC84690	Aec84690 Human cDN
19	735.4	40.6	1727	10 ADA52548	Ada52548 Human cod
20	689.4	38.0	3109	10 ADE47679	Ade47679 Human NOV
21	689.4	38.0	3109	12 ADJ78949	Adj78949 Human NOV
22	689.4	38.0	3109	12 ADJ71668	Adj71668 Human NOV
23	689.4	38.0	3109	12 ADJ71660	Adj71660 Human NOV
24	689.4	38.0	3109	12 ADJ71666	Adj71666 Human NOV
25	687.8	38.0	3109	12 ADJ71664	Adj71664 Human NOV
26	639.8	35.3	1306	12 ADJ71662	Adj71662 Human NOV
27	586.6	32.4	1824	10 ADC35396	Adc35396 Human N-a
28	586.6	32.4	2496	10 ADA52669	Ada52669 Human cod
29	586.6	32.4	2519	9 ACH04034	Ach04034 Human cDN
30	586.6	32.4	2534	6 AAD35232	Aad35232 Human TRN
31	583.4	32.2	2422	10 ADE47689	Ade47689 Human NOV
32	583.4	32.2	2422	10 ADE47687	Ade47687 Human NOV
33	583.4	32.2	2422	10 ADE47685	Ade47685 Human NOV
34	583.4	32.2	2422	12 ADJ78957	Adj78957 Human NOV
35	583.4	32.2	2422	12 ADJ78955	Adj78955 Human NOV
36	583.4	32.2	2422	12 ADJ78959	Adj78959 Human NOV
37	532.4	29.4	534	10 ADE25971	Ade25971 N-acetylgl

38	532.4	29.4	534	14	ADX58234	Adx58234 Human pol
39	476.2	26.3	2465	10	ADB62317	Adb62317 Human cDN
40	424.4	23.4	2388	4	AAI60021	Aai60021 Human pol
41	424.4	23.4	2388	13	ADS11539	Ads11539 Human the
42	422.8	23.3	2416	4	AAI58235	Aai58235 Human pol
43	422.8	23.3	2416	5	ADQ98442	Adq98442 DNA encod
44	422.8	23.3	2416	9	ADB48202	Adb48202 Novel hum
45	402.2	22.2	453	9	ACH40889	Ach40889 Human foe

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 01:13:47 ; Search time 338.51 Seconds
(without alignments)
10015.801 Million cell updates/sec

Title: US-10-713-345-3
Perfect score: 1812
Sequence: 1 atggcgggtggccaggaagat.....tcaaacacgcacggcactga 1812

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1812	100.0	1812	3	US-09-973-457-3 Sequence 3, Appli
2	1812	100.0	2572	3	US-09-973-457-1 Sequence 1, Appli
3	735.4	40.6	1727	4	US-10-094-749-116 Sequence 116, App
4	586.6	32.4	2496	4	US-10-094-749-237 Sequence 237, App
5	476.2	26.3	2465	3	US-10-104-047-471 Sequence 471, App
6	422.8	23.3	2416	3	US-09-620-312D-112 Sequence 112, App
7	368	20.3	903	3	US-09-620-312D-938 Sequence 938, App
8	222.4	12.3	2199	3	US-09-799-451-328 Sequence 328, App
9	208.4	11.5	1540	3	US-09-270-767-11959 Sequence 11959, A
10	204.2	11.3	1920	3	US-09-376-856-1 Sequence 1, Appli
11	204.2	11.3	2575	3	US-10-012-231A-346 Sequence 346, App
12	204.2	11.3	2575	3	US-10-015-389A-346 Sequence 346, App
13	204.2	11.3	2575	3	US-10-006-768A-346 Sequence 346, App
14	204.2	11.3	2575	3	US-10-015-671A-346 Sequence 346, App
15	204.2	11.3	2575	3	US-10-015-393A-346 Sequence 346, App
16	204.2	11.3	2575	3	US-10-011-833A-346 Sequence 346, App
17	204.2	11.3	2575	3	US-10-006-041A-346 Sequence 346, App
18	204.2	11.3	2575	3	US-10-012-064A-346 Sequence 346, App
19	204.2	11.3	2575	4	US-10-015-392A-346 Sequence 346, App
20	204.2	11.3	2575	5	US-10-011-795B-346 Sequence 346, App
21	204.2	11.3	2575	5	US-10-015-386A-346 Sequence 346, App
22	204.2	11.3	2575	5	US-10-012-121A-346 Sequence 346, App
23	204.2	11.3	2575	5	US-10-006-485A-346 Sequence 346, App
24	204.2	11.3	2575	5	US-10-006-746A-346 Sequence 346, App
25	204.2	11.3	2575	5	US-10-012-752A-346 Sequence 346, App
26	204.2	11.3	2575	5	US-10-017-253A-346 Sequence 346, App
27	204.2	11.3	2575	5	US-10-015-519A-346 Sequence 346, App
28	204.2	11.3	2575	5	US-10-015-715A-346 Sequence 346, App
29	204.2	11.3	2575	5	US-10-007-236A-346 Sequence 346, App
30	203.2	11.2	2095	3	US-10-104-047-435 Sequence 435, App
31	202.6	11.2	3332	3	US-09-347-488-1 Sequence 1, Appli
32	190	10.5	740	3	US-09-270-767-27636 Sequence 27636, A
33	186.4	10.3	1521	3	US-09-795-926-30 Sequence 30, Appl
34	186.4	10.3	1521	3	US-10-364-774-30 Sequence 30, Appl
35	186.4	10.3	1812	3	US-09-795-926-42 Sequence 42, Appl
36	186.4	10.3	1812	3	US-10-364-774-42 Sequence 42, Appl
37	186.4	10.3	3896	3	US-09-795-926-44 Sequence 44, Appl
38	186.4	10.3	3896	3	US-10-364-774-44 Sequence 44, Appl
39	171.6	9.5	1746	3	US-10-074-527-3 Sequence 3, Appli
40	171.6	9.5	2850	3	US-10-074-527-1 Sequence 1, Appli
c 41	154.6	8.5	910	3	US-09-270-767-2104 Sequence 2104, Ap
c 42	154.6	8.5	910	3	US-09-270-767-17386 Sequence 17386, A

c	43	144.4	8.0	868	3	US-09-270-767-13764	Sequence 13764, A
	44	137.4	7.6	1771	3	US-09-976-594-28	Sequence 28, Appl
	45	133.2	7.4	810	3	US-09-795-926-26	Sequence 26, Appl

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 01:42:59 ; Search time 2968.06 Seconds
(without alignments)
7501.600 Million cell updates/sec

Title: US-10-713-345-3
Perfect score: 1812
Sequence: 1 atggcggtggccaggaagat.....tcaaacacgcacggcactga 1812

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1812	100.0	1812	3	US-09-973-457-3 Sequence 3, Appli
2	1812	100.0	1812	7	US-10-184-648-44 Sequence 44, Appl
3	1812	100.0	1812	8	US-10-713-345-3 Sequence 3, Appli
4	1812	100.0	2572	3	US-09-973-457-1 Sequence 1, Appli
5	1812	100.0	2572	7	US-10-369-022-15 Sequence 15, Appl
6	1812	100.0	2572	7	US-10-184-648-42 Sequence 42, Appl
7	1812	100.0	2572	8	US-10-713-345-1 Sequence 1, Appli
8	1805.6	99.6	2410	9	US-10-723-860-7517 Sequence 7517, Ap
9	783.4	43.2	1797	6	US-10-060-895A-2 Sequence 2, Appli
10	783.4	43.2	3333	6	US-10-060-895A-1 Sequence 1, Appli
11	783.4	43.2	3439	9	US-10-467-903-21 Sequence 21, Appl
12	744.2	41.1	3183	7	US-10-108-260A-445 Sequence 445, App
13	735.4	40.6	1727	7	US-10-094-749-116 Sequence 116, App
14	689.4	38.0	3109	8	US-10-210-130-41 Sequence 41, Appl
15	689.4	38.0	3109	9	US-10-635-398-61 Sequence 61, Appl
16	689.4	38.0	3109	9	US-10-635-398-67 Sequence 67, Appl
17	689.4	38.0	3109	9	US-10-635-398-69 Sequence 69, Appl
18	687.8	38.0	3109	9	US-10-635-398-65 Sequence 65, Appl
19	639.8	35.3	1306	9	US-10-635-398-63 Sequence 63, Appl
20	586.6	32.4	2496	7	US-10-094-749-237 Sequence 237, App
21	586.6	32.4	2519	6	US-10-116-802-239 Sequence 239, App
22	586.6	32.4	2534	7	US-10-288-252-37 Sequence 37, Appl
23	586.6	32.4	2534	8	US-10-398-038-37 Sequence 37, Appl
24	586.6	32.4	2534	10	US-10-976-440-37 Sequence 37, Appl
25	583.4	32.2	2422	8	US-10-210-130-47 Sequence 47, Appl
26	583.4	32.2	2422	8	US-10-210-130-49 Sequence 49, Appl
27	583.4	32.2	2422	8	US-10-210-130-51 Sequence 51, Appl
28	532.4	29.4	534	7	US-10-292-896-115 Sequence 115, App
29	532.4	29.4	534	9	US-10-705-401-112 Sequence 112, App
30	476.2	26.3	2465	7	US-10-104-047-471 Sequence 471, App
31	476.2	26.3	2465	16	US-11-072-512-471 Sequence 471, App
32	422.8	23.3	2416	6	US-10-037-270-112 Sequence 112, App
33	422.8	23.3	2416	7	US-10-117-722-112 Sequence 112, App
34	422.8	23.3	2416	10	US-10-122-851-112 Sequence 112, App
35	402.2	22.2	453	3	US-09-918-995-28101 Sequence 28101, A
36	368	20.3	903	6	US-10-037-270-938 Sequence 938, App

37	368	20.3	903	7	US-10-117-722-938	Sequence 938, App
38	368	20.3	903	10	US-10-122-851-938	Sequence 938, App
39	353	19.5	1271	8	US-10-276-723-1	Sequence 1, Appli
40	334.8	18.5	580	8	US-10-210-130-43	Sequence 43, Appl
41	292	16.1	757	6	US-10-060-895A-6	Sequence 6, Appli
42	292	16.1	793	6	US-10-060-895A-4	Sequence 4, Appli
43	235.6	13.0	1869	9	US-10-789-241-47	Sequence 47, Appl
44	235.6	13.0	1869	10	US-10-756-149-1870	Sequence 1870, Ap
45	235.6	13.0	2844	6	US-10-098-841-221	Sequence 221, App

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 01:59:47 ; Search time 317.844 Seconds
 (without alignments)
 9113.283 Million cell updates/sec

Title: US-10-713-345-3
 Perfect score: 1812
 Sequence: 1 atggcggtggccaggaagat.....tcaaacacgcacggcactga 1812

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_NA_New:*
 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
 10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
1	1812	100.0	2572	8	US-11-312-958-15	Sequence 15, Appl
2	783.4	43.2	3298	8	US-11-266-748A-56451	Sequence 56451, A
3	744.2	41.1	3183	8	US-11-293-697-445	Sequence 445, App
4	586.6	32.4	2519	8	US-11-266-748A-31678	Sequence 31678, A
5	586.6	32.4	2519	8	US-11-266-748A-56113	Sequence 56113, A
6	454	25.1	794	8	US-11-266-748A-1713	Sequence 1713, Ap
7	370	20.4	2135	8	US-11-266-748A-23941	Sequence 23941, A
8	370	20.4	2135	8	US-11-266-748A-57086	Sequence 57086, A
9	316.2	17.5	920	8	US-11-266-748A-190028	Sequence 190028,
10	236.8	13.1	1000	8	US-11-266-748A-406202	Sequence 406202,
c 11	236.8	13.1	1000	8	US-11-266-748A-477248	Sequence 477248,
c 12	235.6	13.0	2332	8	US-11-266-748A-189071	Sequence 189071,
13	235.6	13.0	2332	8	US-11-266-748A-242737	Sequence 242737,
14	235.6	13.0	2819	8	US-11-266-748A-27039	Sequence 27039, A
15	204.2	11.3	2575	6	US-10-196-749-363	Sequence 363, App
16	204.2	11.3	3580	8	US-11-266-748A-56877	Sequence 56877, A
17	186.4	10.3	5222	8	US-11-266-748A-31657	Sequence 31657, A
18	184.4	10.2	3105	8	US-11-293-697-336	Sequence 336, App
19	173.8	9.6	1163	8	US-11-266-748A-367663	Sequence 367663,
c 20	173.8	9.6	1163	8	US-11-266-748A-451042	Sequence 451042,
21	170	9.4	1746	8	US-11-266-748A-22604	Sequence 22604, A
22	165.4	9.1	1542	8	US-11-266-748A-188164	Sequence 188164,
23	165.4	9.1	4464	8	US-11-266-748A-27336	Sequence 27336, A
24	164.4	9.1	650	7	US-11-190-172-4285	Sequence 4285, Ap
25	151.8	8.4	1140	8	US-11-266-748A-96859	Sequence 96859, A
c 26	151.8	8.4	1140	8	US-11-266-748A-149670	Sequence 149670,
27	135.4	7.5	5360	8	US-11-266-748A-57295	Sequence 57295, A
28	131.4	7.3	1635	8	US-11-266-748A-183850	Sequence 183850,
c 29	128.4	7.1	968	8	US-11-266-748A-370880	Sequence 370880,
30	128.4	7.1	968	8	US-11-266-748A-454259	Sequence 454259,
31	119.8	6.6	2185	8	US-11-221-332-109	Sequence 109, App
32	117	6.5	818	8	US-11-266-748A-356278	Sequence 356278,
33	117	6.5	818	8	US-11-266-748A-385814	Sequence 385814,
c 34	117	6.5	818	8	US-11-266-748A-439657	Sequence 439657,
c 35	111	6.1	769	8	US-11-266-748A-259798	Sequence 259798,
c 36	111	6.1	769	8	US-11-266-748A-279021	Sequence 279021,
37	111	6.1	769	8	US-11-266-748A-320315	Sequence 320315,
38	104	5.7	1000	8	US-11-266-748A-399106	Sequence 399106,
c 39	104	5.7	1000	8	US-11-266-748A-470152	Sequence 470152,
40	103.8	5.7	1066	8	US-11-266-748A-360857	Sequence 360857,
c 41	103.8	5.7	1066	8	US-11-266-748A-444236	Sequence 444236,
42	103	5.7	862	8	US-11-266-748A-98276	Sequence 98276, A

c	43	103	5.7	862	8	US-11-266-748A-151087	Sequence 151087,
	44	96.4	5.3	869	8	US-11-266-748A-98384	Sequence 98384, A
c	45	96.4	5.3	869	8	US-11-266-748A-151195	Sequence 151195,

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 00:50:04 ; Search time 8655.77 Seconds
 (without alignments)
 11706.157 Million cell updates/sec

Title: US-10-713-345-3
 Perfect score: 1812
 Sequence: 1 atggcgggtggccaggaagat.....tcaaacacgcacggcactga 1812

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*
 1: gb_est1:*
 2: gb_est3:*
 3: gb_est4:*
 4: gb_est5:*
 5: gb_est6:*
 6: gb_htc:*
 7: gb_est2:*
 8: gb_est7:*
 9: gb_est8:*
 10: gb_est9:*
 11: gb_gss1:*
 12: gb_gss2:*
 13: gb_gss3:*
 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1373.8	75.8	2886	6	AK032568	AK032568 Mus muscu
2	1180.8	65.2	1368	14	DQ048170	DQ048170 Homo sapi
3	838.8	46.3	1056	3	BM925654	BM925654 AGENCOURT
4	813.2	44.9	1322	14	DQ048171	DQ048171 Pan trogl
5	783.4	43.2	1797	14	AY407808	AY407808 Homo sapi
6	755.4	41.7	1797	14	AY407810	AY407810 Mus muscu
7	732	40.4	879	2	BI756878	BI756878 603029069
8	720.4	39.8	866	10	DV913368	DV913368 LB02827.C
9	717.6	39.6	1120	3	BM907000	BM907000 AGENCOURT
10	696	38.4	761	2	BI822362	BI822362 603037922
11	676.6	37.3	806	8	CO886915	CO886915 BovGen_15
12	675.6	37.3	839	5	CJ470325	CJ470325 CJ470325
13	645	35.6	1016	10	DV011836	DV011836 CNB271-C0
14	620.8	34.3	624	4	CB152086	CB152086 K-EST0209
15	616.8	34.0	782	8	CN823582	CN823582 Oa_splbn_
16	610.4	33.7	2031	6	AK048758	AK048758 Mus muscu
17	604.8	33.4	652	5	CD630910	CD630910 56006229J
18	602.4	33.2	1797	14	AY407809	AY407809 Pan trogl
19	598.2	33.0	793	2	BI552481	BI552481 603196186
20	593.8	32.8	1990	6	AK035817	AK035817 Mus muscu
21	591	32.6	2617	6	AK051281	AK051281 Mus muscu
22	588.4	32.5	596	9	DR001000	DR001000 TC112896
23	588	32.5	588	9	DA406079	DA406079 DA406079
24	582.4	32.1	596	9	DA586340	DA586340 DA586340
25	580.4	32.0	1541	6	AK171529	AK171529 Mus muscu
26	580	32.0	580	9	DA064328	DA064328 DA064328
27	574.4	31.7	576	9	DA079387	DA079387 DA079387
28	574	31.7	574	9	DA086071	DA086071 DA086071
29	564	31.1	564	9	DA077079	DA077079 DA077079
30	561	31.0	561	9	DA201413	DA201413 DA201413
31	560.4	30.9	562	9	DA355587	DA355587 DA355587
32	551.4	30.4	553	9	DA122336	DA122336 DA122336
33	533.4	29.4	1578	6	AK170381	AK170381 Mus muscu
34	526.2	29.0	531	4	CB154648	CB154648 K-EST0212
35	522.6	28.8	1019	2	BM543465	BM543465 AGENCOURT
36	519	28.6	555	9	DA074160	DA074160 DA074160
37	519	28.6	825	3	BU458046	BU458046 603776544
38	516.6	28.5	1046	10	DW666789	DW666789 CNB338-H1

39	513.4	28.3	525	9	DA624069	DA624069	DA624069
40	512.8	28.3	517	4	CB153078	CB153078	K-EST0210
41	506.4	27.9	780	3	BU385765	BU385765	603861678
42	499.8	27.6	814	5	CJ430976	CJ430976	CJ430976
43	491.6	27.1	889	10	DV868862	DV868862	LB0251.CR
44	490.8	27.1	1048	9	DN684343	DN684343	CGX35-D06
45	486.2	26.8	990	3	BU273821	BU273821	603531731